

SEARCH REQUEST FORM
Scientific and Technical Information Center

Requester's Full Name: JANE ZACH Examiner #: 77512 Date: 11-30-07
 Art Unit: 1635 Phone Number 301-2-0765 Serial Number: 071903,165
 Mail Box and Bldg/Room Location: 2728 Results Format Preferred (circle): PAPER DISK E-MAIL
2C18

If more than one search is submitted, please prioritize searches in order of need. MEJ

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Mutant B types

Inventors (please provide full names): Sobel et al.

Earliest Priority Filing Date: 3-9-01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search Seq ID No: 34
AA-774

AA Databases ab MEJ

No size limits

Please Search for Interference
of regular date
Results

Thanks

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher:		NA Sequence (#)	STN _____
Searcher Phone #:		AA Sequence (#)	Dialog _____
Searcher Location:		Structure (#)	Questel/Orbit _____
Date Searcher Picked Up:	<u>12/11/07</u>	Bibliographic	Dr. Link _____
Date Completed:		Litigation	Lexis/Nexis _____
Searcher Prep & Review Time:		Fulltext	Sequence Systems <u>RDP</u> _____
Clerical Prep Time:		Patent Family	WWW/Internet _____
Online Time:		Other	Other (specify) _____

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CM protein - protein search, using sw model

Run on:

December 1, 2004, 16:20:27 ; Search time 161 Seconds

{without alignments}

1.724.574 Million cell updates/sec

Title: US-09-803-165-34

Perfect score: 4026

Sequence: 1.NIFDTPTVITKDGKPIIRKF.....REDLRLYQSSKQVGGLDAWLRK 774

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 200273 seqs, 35829299 residues

Total number of hits satisfying chosen parameters: 200273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_GeneSeq_21Sep04:*

1: geneseqP19809:*

2: geneseqP19908:*

3: geneseqP20008:*

4: geneseqP20018:*

5: geneseqP20026:*

6: geneseqP20038:*

7: geneseqP20048:*

8: geneseqP20049:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 4026 100.0 774 5 ADG7991

2 3990 95.1 774 2 ADW2323

3 3840 95.4 774 7 ADG45207

4 3840 95.4 774 7 ADG64509

5 3840 95.4 774 8 ADN75098

6 3835 95.3 774 7 ADG42210

7 3835 95.3 774 7 ADG5213

8 3834 95.2 774 7 ADG5215

9 3834 95.2 774 7 ADG5240

10 3834 95.2 774 7 ADG5242

11 3834 95.2 774 8 ADG5205

12 3833 95.2 774 7 ADG4241

13 3833 95.2 774 8 ADG8204

14 3832 95.2 774 7 ADG5216

15 3832 95.2 774 7 ADG45209

16 3832 95.2 774 7 ADG45209

17 3832 95.2 774 7 ADG4211

18 3832 95.2 774 7 ADG5214

19 3831 95.2 774 7 ADG5212

20 3831 95.2 774 7 ADG5239

21 3831 95.2 774 7 ADG42208

22 3829 95.1 774 8 ADM13792

23 3446.5 85.6 1829 2 ADW9322

24 3446.5 85.6 1829 8 ADN5952

25 3356.4 83.4 1702 8 ADR38095

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: geneseqP19809:*

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3: geneseqP20008:*

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6 3835 95.3 774 7 ADG42210

7 3835 95.3 774 7 ADG5213

8 3834 95.2 774 7 ADG5215

9 3834 95.2 774 7 ADG5240

10 3834 95.2 774 7 ADG5242

11 3834 95.2 774 8 ADG5205

12 3833 95.2 774 7 ADG4241

13 3833 95.2 774 8 ADG8204

14 3832 95.2 774 7 ADG5216

15 3832 95.2 774 7 ADG45209

16 3832 95.2 774 7 ADG45209

17 3832 95.2 774 7 ADG4211

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19 3831 95.2 774 7 ADG5212

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15 3832 95.2 774 7 ADG45209

16 3832 95.2 774 7 ADG45209

17 3832 95.2 774 7 ADG45211

18 3832 95.2 774 7 ADG5214

19 3831 95.2 774 7 ADG5212

20 3831 95.2 774 7 ADG5239

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10 3834 95.2 774 7 ADG5242

11 3834 95.2 774 8 ADG5205

12 3833 95.2 774 7 ADG4241

Matches	774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	PP	25-MAR-1995;	96DB-01011759.
QY	1 MIFDDYITDGKPTIRIKRKENGEFKIELDPHQPYIVALLKDSATDEKAIGERHG 60	XX	PR	25-MAR-1996;	96DB-01011759.
Db	1 MIFDDYITDGKPTIRIKRKENGEFKIELDPHQPYIVALLKDSATDEKAIGERHG 60	XX	PA	(BOEP) BOHRINGER MANNHEIM GMBH.	
QY	61 KIVRVVDAVKKKELGRDVEWKUFLERPDVALKRKRERPAVIDTYEVDIPAKRY 120	XX	PI	Frey B, Niehaus F, Antranikian G,	
Db	61 KIVRVVDAVKKKELGRDVEWKUFLERPDVALKRKRERPAVIDTYEVDIPAKRY 120	XX	DR	WPI; 1997-481494/45.	
QY	121 LIDKGILPMGDEBKLKMAFDIETYHEGDFGKEIMISYADEBARVITWNIDPY 180	XX	N-PSDB; AATB6434.		
Db	121 LIDKGILPMGDEBKLKMAFDIETYHEGDFGKEIMISYADEBARVITWNIDPY 180	XX	PT	Thermstable DNA Polymerase from Thermococcus sp. TY - useful for nucleic acid amplification.	
QY	181 VDVSNREMKRKFVQVREKDPDYLITGDNFDPYLKRAEKGVLILLGRKERVE 240	XX	PS	Claim 1; Page 9-10; 32pp; German.	
Db	181 VDVSNREMKRKFVQVREKDPDYLITGDNFDPYLKRAEKGVLILLGRKERVE 240	XX	CC	The present sequence (TY Bixon) is a Thermococcus sp. TY (DSM 10597) thermostable DNA polymerase with 3'-5' exonuclease activity. The enzyme can specifically amplify nucleic acid fragments of up to 5 kb in high yields, has an activity half-life of 20 minutes at 90 degrees C, has an optimum temperature of 70-80 degrees C, has an optimum pH of 7.5, exhibits optimum activity at a KCl concentration of 80-100 mM, is magnesium ion-dependent and is inhibited by manganese ions	
Db	301 WETESMKKKLQYSMEDARATYELGEKPFMEABLKLQGSVNDVSRSTGNVETWL 360	CC	CC		
Db	301 WETESMKKKLQYSMEDARATYELGEKPFMEABLKLQGSVNDVSRSTGNVETWL 360	CC	CC		
QY	361 RVAVERELAPNPKPDPBEYRRLRTYLGIVKPERGLMENILDFCLYPSLWTHN 420	CC	SQ	Sequence 774 AA;	
Db	361 RVAVERELAPNPKPDPBEYRRLRTYLGIVKPERGLMENILDFCLYPSLWTHN 420	CC	Query Match 99.1%; Score 3990; DB 2; Length 774; Best Local Similarity 99.4%; Pred. No. 2.7e-302; Matches 769; Conservative 1; Mismatches 4; Indels 0; Gaps 0;		
QY	421 VSPDTLREGCKNYDVAIPVGKCKDPGPFPISPLGENTYRDKKKKATIDPEKK 480	Db	QY 1 MIFDDYITDGKPTIRIKRKENGEFKIELDPHQPYIVALLKDSATDEKAIGERHG 60		
Db	421 VSPDTLREGCKNYDVAIPVGKCKDPGPFPISPLGENTYRDKKKKATIDPEKK 480	Db	1 MIFDDYITDGKPTIRIKRKENGEFKIELDPHQPYIVALLKDSATDEKAIGERHG 60		
QY	481 MLDYRQAVKLLANSYGYMGPKARYSCEASVTANGRHYEMTIKEIEBKCFKVL 540	Db	QY 61 KIVRVVDAVKKKELGRDVEWKUFLERPDVALKRKRERPAVIDTYEVDIPAKRY 120		
Db	481 MLDYRQAVKLLANSYGYMGPKARYSCEASVTANGRHYEMTIKEIEBKCFKVL 540	Db	61 KIVRVVDAVKKKELGRDVEWKUFLERPDVALKRKRERPAVIDTYEVDIPAKRY 120		
QY	541 YADTDGFYATIPGEKPTIKKAKEFLKYINSKULGILIBYEGFYLRGFVAKRYVTL 600	Db	QY 121 LIDKGILPMGDEBKLKMAFDIETYHEGDFGKEIMISYADEBARVITWNIDPY 180		
Db	541 YADTDGFYATIPGEKPTIKKAKEFLKYINSKULGILIBYEGFYLRGFVAKRYVTL 600	Db	121 LIDKGILPMGDEBKLKMAFDIETYHEGDFGKEIMISYADEBARVITWNIDPY 180		
QY	601 DSEGRTTRLEVERWDWSLSEAKETOAKVIAEILKEDSYTAKAELVWEEAKYQPL 660	Db	QY 301 WETESMKKKLQYSMEDARATYELGEKPFMEABLKLQGSVNDVSRSTGNVETWL 360		
Db	601 DSEGRTTRLEVERWDWSLSEAKETOAKVIAEILKEDSYTAKAELVWEEAKYQPL 660	Db	301 WETESMKKKLQYSMEDARATYELGEKPFMEABLKLQGSVNDVSRSTGNVETWL 360		
QY	601 DSEGRTTRLEVERWDWSLSEAKETOAKVIAEILKEDSYTAKAELVWEEAKYQPL 660	Db	QY 181 VDVSNREMKRKFVQVREKDPDYLITGDNFDPYLKRAEKGVLILLGRDPE 240		
Db	601 DSEGRTTRLEVERWDWSLSEAKETOAKVIAEILKEDSYTAKAELVWEEAKYQPL 660	Db	181 VDVSNREMKRKFVQVREKDPDYLITGDNFDPYLKRAEKGVLILLGRDPE 240		
QY	661 EKLVTHQQTDLISYKAIGPHVATAKLAAGKURPOTISIVLGSKISDRVILL 720	Db	QY 241 PKHRMDSFAVIKGRHFDPVURTINLPYTLAEVAGTKSKGABBAII 300		
Db	661 EKLVTHQQTDLISYKAIGPHVATAKLAAGKURPOTISIVLGSKISDRVILL 720	Db	241 PKHRMDSFAVIKGRHFDPVURTINLPYTLAEVAGTKSKGABBAII 300		
QY	721 SEYPKKHKDPPYTENQDPAVRLIEFGYKEDLKQSSQVGLDWWLKK 774	Db	QY 301 WETESMKKKLQYSMEDARATYELGEKPFMEABLKLQGSVNDVSRSTGNVETWL 360		
Db	721 SEYPKKHKDPPYTENQDPAVRLIEFGYKEDLKQSSQVGLDWWLKK 774	Db	301 WETESMKKKLQYSMEDARATYELGEKPFMEABLKLQGSVNDVSRSTGNVETWL 360		
RESULT 2		QY	361 RVAVERELAPNPKPDPBEYRRLRTYLGIVKPERGLMENILDFCLYPSLWTHN 420		
ID AAW9323	AAW9323 standard; protein; 774 AA.	Db	361 RVAVERELAPNPKPDPBEYRRLRTYLGIVKPERGLMENILDFCLYPSLWTHN 420		
AC AAW9323;		QY	421 VSPDTLREGCKNYDVAIPVGKCKDPGPFPISPLGENTYRDKKKKATIDPEKK 480		
DT 20-APR-1998 (first entry)		Db	421 VSPDTLREGCKNYDVAIPVGKCKDPGPFPISPLGENTYRDKKKKATIDPEKK 480		
XX	DNA Polymerase with 3'-5' exonuclease activity.	QY	481 MLDYRQAVKLLANSYGYMGPKARYSCEASVTANGRHYEMTIKEIEBKCFKVL 540		
XX	DNA Polymerase with 3'-5' exonuclease activity.	Db	541 YADTDGFYATIPGEKPTIKKAKEFLKYINSKULGILIBYEGFYLRGFVAKRYVTL 600		
XX	DNA Polymerase with 3'-5' exonuclease activity.	QY	601 DSEGRTTRLEVERWDWSLSEAKETOAKVIAEILKEDSYTAKAELVWEEAKYQPL 660		
OS Thermococcus sp.		Db			
XX		QY			
PN DEL611729-A1.		Db			
XX		QY			
PD 02-OCT-1997.		Db			

Autocatalytic cleavage; DNA replication; DNA-binding;
KW DNA-directed DNA Polymerase; Endonuclease; Hydrolase;
KW Protein splicing; Transferase.
PT CHAIN 1 409 DNA polymerase, 1st part (Potential).
PT CHAIN 410 769 Intein I.
PT CHAIN 770 855 DNA polymerase, 2nd part (Potential).
PT CHAIN 856 1392 Intein II.
PT CHAIN 1393 1441 DNA polymerase, 3rd part (Potential).
PT CHAIN 1442 1598 Intein III.
PT CHAIN 1599 1829 DNA polymerase, 4th part (Potential).
SQ SEQUENCE 1829 AA; 211875 MW; A11348BC57EB9C03 CRC54;

Query Match 85.6%; Score 3446.5; DB 1; length 1829;
Best Local Similarity 42.2%; Pred. No. 9.8e-177; Matches 771; Conservative 0; Mismatches 3; Indels 1055; Gaps 3;

QY 1 MIFDTDYITDKGKPIRIFPKENGKFGKISDPHFOPYTIAKIKODSATDEKALKGERG 60
Db 1 MILDPTYITDKGKPIRIFPKENGKFGKISDPHFOPYTIAKIKODSATDEKALKGERG 60
QY 61 KIVRVDVAKVKKKLGDRDVVKLIFEARQDVAFLRGKREHAPAVIDYEVKIPFARY 120
Db 61 KIVRVDVAKVKKKLGDRDVVKLIFEARQDVAFLRGKREHAPAVIDYEVKIPFARY 120
QY 121 LIDKGLPMGDEEKLMLADIETYHEGDFGKOBIMSYADBEARWITWNKIDPY 180
Db 121 LIDKGLPMGDEEKLMLADIETYHEGDFGKOBIMSYADBEARWITWNKIDPY 180
QY 181 VDVVSNBREMKRFQVIRSKPDVLITYNGDNFDLPIYLKRAKLGVTLLGRDKEPE 240
Db 181 VDVVSNBREMKRFQVIRSKPDVLITYNGDNFDLPIYLKRAKLGVTLLGRDKEPE 240
QY 241 PKIHRMGDSAVEIKRIGHDLFPVVRTINLPYTLAEVANLGKSKGABEAI 300
Db 241 PKIHRMGDSAVEIKRIGHDLFPVVRTINLPYTLAEVANLGKSKGABEAI 300
QY 301 WTEESMKKLAQYSMEDARATVYELGEFFNNEAHLIGOSMWDNSRSTGNVEWILL 360
Db 301 WTEESMKKLAQYSMEDARATVYELGEFFNNEAHLIGOSMWDNSRSTGNVEWILL 360
QY 361 RVAYEENBIAKPKPDEEYRRRLRTYLSGTYKEPERGWIENITYLDPRC 410
Db 361 RVAYEENBIAKPKPDEEYRRRLRTYLSGTYKEPERGWIENITYLDPRC 410
QY 411 RUAVERNLBAPNKDDEBIRKLRTYLGGSYKSFPERGIANIYDFFCRHPADTKVK 410
Db 411 RUAVERNLBAPNKDDEBIRKLRTYLGGSYKSFPERGIANIYDFFCRHPADTKVK 410
QY 421 GKGIVNISDVKGVDGYTIGIDOWQVRERKVWVHYEGKLININGLKCTPNHKUPVVTENDQ 480
Db 421 GKGIVNISDVKGVDGYTIGIDOWQVRERKVWVHYEGKLININGLKCTPNHKUPVVTENDQ 480
QY 411 - 410
Db 411 - 410
QY 481 TRIDSILAKSFLSGKVKGKLTTPKEKIAFEKPKSEEEILKGBLSGTILAEGLRK 540
Db 411 - 410
QY 541 DIEYFSSRKRKRISHQYRPRITIGENBELLERIYIPLKLFPGTRPSVKGDNALKI 600
Db 411 - 410
QY 601 TPAKAVYQIBELLKNIESLYAPAVTRGFPPERDATVNKRSTIVTWTQHNWKDITVA 660
Db 411 - 410
QY 661 KLLDSLGIPSYRSYEVKVIENCKELTKHILITGRDGLILQTYGFISSRNKALEKAE 720
Db 411 - 410
QY 721 VREMNLKNNPFYNTLSEFSEVYKGVWVDTLSGNYPPVANGLTHNLSLYPSIVHN 780
Db 421 VSPDTTREGCKYDVAIVSYKFCKDPPGPISTGELTMQRQIKKOMATDPISK 480
Db 781 VSPDTTREGCKYDVAIVSYKFCKDPPGPISTGELTMQRQIKKOMATDPISK 840
Db 481 MLDYGRPAVKLIA-----

RESULT 2

DPOI_ THRLI

ID _DPOI_ THRLI

STANDARD;

PRT;

1702 AA.

AC P30317;

DT 01-APR-1993 (Rel. 25, Created)

OM protein - protein search, using SW model
 Run on: December 1, 2004, 16:23:42 ; Search time 21 Seconds
 Sequence: US-09-803-165-34
 Perfect score: 4026
 Scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_79;*
 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	3356	83.4	1702	2	S42459
2	3204.5	79.6	57920	2	DNA-directed DNA polymerase (EC 2.7.7.7) Vent, intein containing precursor - Thermococcus litorialis
3	3164.5	78.6	771	2	C75023
4	3151.5	78.3	775	2	S35543
5	2934.5	72.9	1312	2	S68593
6	2886	71.7	1235	2	C71210
7	2764.5	68.7	1670	2	S71512
8	1301	32.3	781	2	E69312
9	1291	32.1	1634	2	E64410
10	1209.5	30.9	586	2	C69028
11	1204.5	29.9	781	2	JCT7382
12	1190	29.6	803	2	B56277
13	1138	28.3	784	2	E72515
14	693.5	17.2	1088	2	T05731
15	676.5	16.8	764	2	S75407
16	659.5	16.4	1038	1	JCS577
17	657.5	16.3	1038	2	T18222
18	657.5	16.3	1086	2	C70242
19	649.5	16.1	1086	2	E74266
20	626	15.5	901	2	E84210
21	621.5	15.4	1097	1	RNB13
22	619.5	15.4	882	2	S23019
23	619.5	15.4	1084	1	S19661
24	615.5	15.3	872	2	JCT7380
25	616.5	15.3	882	2	F90201
26	616.5	15.3	1105	1	S02423
27	614.5	15.3	1094	2	S22573
28	611	15.2	1107	1	A41618
29	609	15.1	1513	2	T2B158

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 GenCore version 5.1.6
 (without alignments)
 3546.275 Million cell updates/sec

Scoring table:

Searched:

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Db	1	MILDYDITDKGKPIRFRKENGKFKEFLDPHQPYIYALLKDDSAIBERKAIGERHG	Db	1081	DVSGESBIIIRQNGKIRPKIKOLPESKVYSIGKEYCILEGEALTLDDGGKUVWKPV
Qy	61	KIVRVDAVKVKKEFLGRDVEWKLIPEHQDPALRKTRHAPIVYDIPFAKRY	Qy	544	-----
Db	61	KTVVILDAVKRKFLGREVEWNLIFSEHQDPAMRKCKREPAWDIYEVDIPFAKRY	Db	1141	PYMRERHANKRMFRIMLINSWIDTEDHSLSIGINTSKTAKKIGERIKEVKPFLGK
Qy	121	LIDKGLIPMBGDEELKUMARDFHYHEDGFGRGBINISYADEBEARVITKNIDPY	Qy	544	-----
Db	121	LIDKGLIPMBGDEELKUMARDFHYHEDGFGRGBINISYADEBEARVITKNIDPY	Db	1201	AVSLICPNAPIKDENTTSIAVKEWNLISVGDRNGGDSRABYIYLSTGKDAE
Qy	181	VDVMSNEREMIKRFQVVKEDKPDVLTINGDNFDLPIYIKRAKGUTLLGRDKEPE	Qy	544	-----
Db	181	VDVMSNEREMIKRFQVVKEDKPDVLTINGDNFDLPIYIKRAKGUTLLGRDKEPE	Db	1261	IKQKLAPBLKTYGVISNYPPKNEKGDPNITAKSLVFKMFRHPDKERKRPPEMELPV
Qy	241	PKIHMRGDSAAVEIKGRHRDLPFPVRNTLNPLPTBAVYZAVTGKTKSKGABELAI	Qy	544	-----
Db	241	PKIHMRGDSAAVEIKGRHRDLPFPVRNTLNPLPTBAVYZAVTGKTKSKGABELAI	Db	1321	TYEARFLRGIFSADGTIVRKGVPEIRLNTIDADFLRBRVRLWTVGISNSIAETPNR
Db	241	PKIQAMGDSAAVEIKGRHRDLPFPVRNTLNPLPTBAVYZAVTGKTKSKGABELAI	Qy	544	-----
Qy	301	WETRESMKKLAQSYNSDARATYSLCKEFPMEEASLAKLIGQSVDSSSTGVLVENTL	Db	1380	1.61 YNGVSTCTYSHLRIRNKWFAERTIGPLIERKQRKLUHLKSARVAKNTIDFGPDLMVHK
Db	301	WETRESMKKLAQSYNSDARATYSLCKEFPMEEASLAKLIGQSVDSSSTGVLVENTL	Qy	544	-----
Qy	361	RVAYERNELAQNPKPBBEYRIRRTYLGYYKPERGMENTYDRCYLXSIYHN	Db	1441	KUBIPFEGYVWIDEVWETHFFANMILNHNDGPATIPERKPELKICKKAEPLNTS
Db	361	RVAYERNELAQNPKPBBEYRIRRTYLGYYKPERGMENTYDRCYLXSIYHN	Qy	544	-----
Qy	421	VSPDTLEKBCGKNDYVAIPGVRCKDPFPPIPSIGETIMREIKKOMATDIEKK	Db	1573	KLPGLULIYEYRPFYLRGPFVAKRYVATIDEGRITTRGLEYTRDRMSBIAKETOAKLSEA
Db	421	VSPDTLEKBCGKNDYVAIPGVRCKDPFPPIPSIGETIMREIKKOMATDIEKK	Qy	572	632 KUPLGLULIYEYRPFYLRGPFVAKRYVATIDEGRITTRGLEYTRDRMSBIAKETOAKLSEA
Qy	481	MLDYQRORAKVLA-----	Db	1501	1501 KUPLGLULIYEYRPFYLRGPFVAKRYVATIDEGRITTRGLEYTRDRMSBIAKETOAKLSEA
Db	481	MLDYQRORAKVLA-----	Qy	1500	1500 KUPLGLULIYEYRPFYLRGPFVAKRYVATIDEGRITTRGLEYTRDRMSBIAKETOAKLSEA
Qy	494	-----	Db	1621	633 LIKEDSTEKAVIWKVTEAKYOTPLEKUVIHSOIKSEYKAGIHPYIAKRLAAK
Db	541	VNLNFAPSFKKIKSEVKUKALIRHKYKAVELQIUSSGRKINTAGHSLFTVNGEI	Qy	1620	1620 ILKEGSVKAVVDRVKEVAKYRVELEKVKVHEQITRDQKDGKAGPHVIAKRLAAK
Qy	494	-----	Db	693	693 GIKRPETIISIVLGSKGSKSDRVILSEYDPKKEDYDPUYIENQVLPVRLIAFG
Db	601	KEVSGDGKIKEGLDLIVAPKKIKNEKOVINSINIPELSLDSEEETADIVMTISAKORKNAFK	Qy	752	752 GIKRPETIISIVLGSKGSKSDRVILSEYDPKKEDYDPUYIENQVLPVRLIAFG
Qy	494	-----	Db	1681	1681 YRKEDDRIYQSSKQGTLGAWLR
Db	661	GMLRLTRWMFGBENRIFTNRYLFHLEKGLIKULPRGEVTDWERLKRYKOLYKLAG	Db	1680	1680 1621 GIKRPETIISIVLGSKGSKSDRVILSEYDPKKEDYDPUYIENQVLPVRLIAFG
Qy	494	-----	Qy	774	774 1621 GIKRPETIISIVLGSKGSKSDRVILSEYDPKKEDYDPUYIENQVLPVRLIAFG
Db	721	SVKYNGKIRBYLWENEBIKDPISYPOKELLBWKIGTLNGPRTMCLVKDVFEGKLLAY	Db	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Qy	494	-----	Db	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Db	781	VSEGYAGAQKNTGGISYSVLYNEDPNVLSRSMKAVASKEFGKRVDRNVCISKRMAYL	Db	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Qy	494	-----	Qy	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Db	841	VMKCLGALAKENKRIPSVILTSPEPVWSTLEAVFTGDIHPSKFRISTKSLLANQI	Db	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Qy	494	-----	Db	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Db	901	VFLNSLIGISSVKGIGDSCVTRVITNEDLQPTSRKNTYMSNLPKRLDUGKRCQ	Db	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Qy	494	-----	Qy	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Db	961	KMVKFKFKFLVDGKLNRERAKLLEFFINGDIVIDRVKSVKEDYVTDLSVEDNEI	Db	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Qy	494	-----	Db	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Db	1021	FLVGFGLIYAHNSYGYGNGYKPARWISKEAESVIAWGRHTIENTIREBEKFGPKVLYA	Qy	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR
Qy	543	D-----	Db	493	493 1620 1680 1681 YRKEDDRIYQSSKQGTLGAWLR

RESULT 2

S67920

DNA-directed DNA polymerase (EC 2.7.7.7) - Thermococcus sp.

C.Species:

Thermococcus sp.

C.Sequence:

#sequence_revision 13-Mar-1998 #text_change 09-Jul-2004

C.Accession:

S67920

R.Southworth, M.S.; Kong, R.; Kucera, R.B.; Ware, J.; Jannasch, H.W.; Berlin, F.B.

Submitted to the

EMBL

Library, January 1996

A.Description:

Cloning, expression, and modulation of the 3'-5' exonuclease activity of

A.Reference number:

S67920

A.Accession:

S67920

A.Molecule type:

DNA

A.Residues:

1-175 <SOI>

A;Cross-references:

UniProt:Q56366; GB:U47108; PID:91197451; PID:AAA86769.1; PID:91197452

C.Experimental source:

strain 90N-7

C.Superfamily:

DNA polymerase

C.Keywords:

DNA binding; nucleotidyltransferase

Query Match

79.6%

Score 3204.5;

DB 2;

Length 775;

Best Local Similarity

75.6%;

Pred. No. 9

4e-159;

Indels 3;

Gaps 2;

Matches 592;

Conservative 89;

Mismatches 89;

Indels 3;

Gaps 2;

Best Local Similarity

75.6%;

Pred. No. 9

4e-159;

Indels 3;

Gaps 2;

Matches 592;

Conservative 89;

Mismatches 89;

Indels 3;

Gaps 2;

Best Local Similarity

75.6%;

Pred. No. 9

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